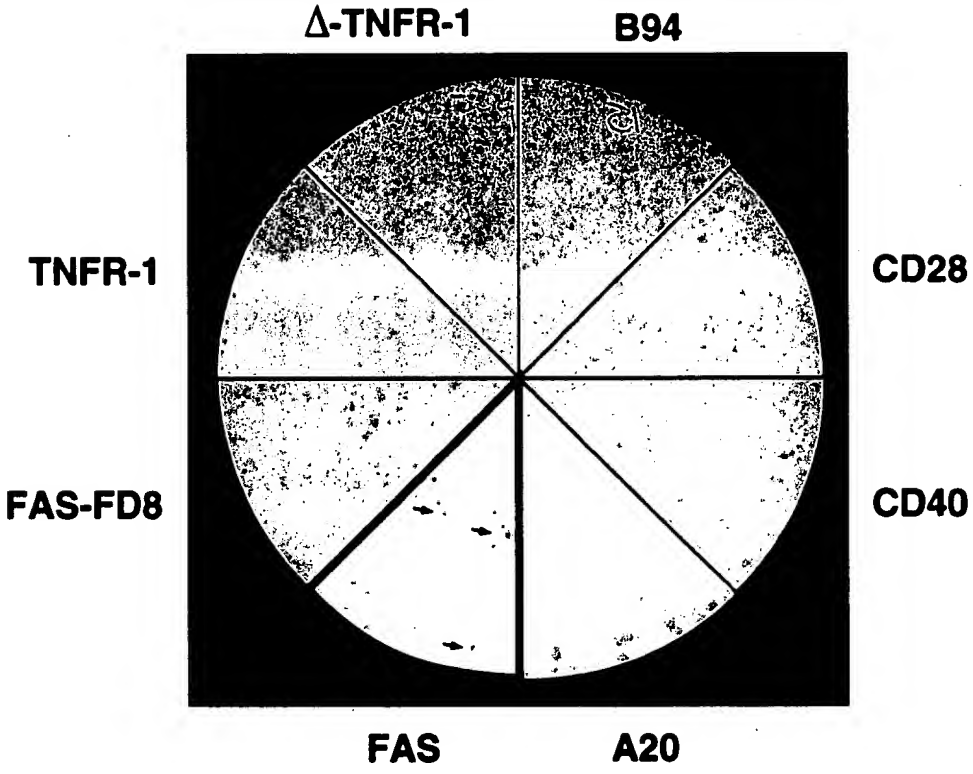

FIG. 1

```
CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG

                                                100
GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA

GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC
         Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser

                                                200  CLONE 15
AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG
Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly

                                                        CLONE 8
CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu

                                                    300
TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu

CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg

                                                        400
CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly

GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly

                                                    ▽       500
AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys

ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val

                                                            600
CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr

GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val

GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
```

FIG. 2A

```
  700
AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser


GAA GCG TCC TGA TGGGCCGCTG CTTTGCGCTG GTGGACCACA GGCATCTACA
Glu Ala Ser  *

 800
CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA

                                                    900
GCCAGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCGTT TATTAATGCC


TCTCCCGCAC CAGGCCGGGC TTGGGCCCTG CACAGATATT TCCATTTCTT CCTCACTATG

                         1000
ACACTGAGCA AGATCTTGTC TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG


AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC

1100
GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAAGC AGAGAGGTGG AGAACTGGGA

                                                    1200
TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTCAAC CACTGTGGCG TTCTGCTGCC


CCTGCAGTTG GCAGAAAGGA TGTTTTGTCC CATTTCCTTG GAGGCCACCG GGACAGACCT

                         1300
GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG


GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCCTGTGT GAGTTGAGTC TCCTCTCTGA

1400
GACTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG

                                                    1500
CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCCTG


CAATTCTACA GTTTCTTACT GTTTTGTATC AAAATCACTA TCTTTCTGAT AACAGAATTG

                         1600
CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCTAA GGTAATCCTA

TTAAAA
```

FIG. 2B

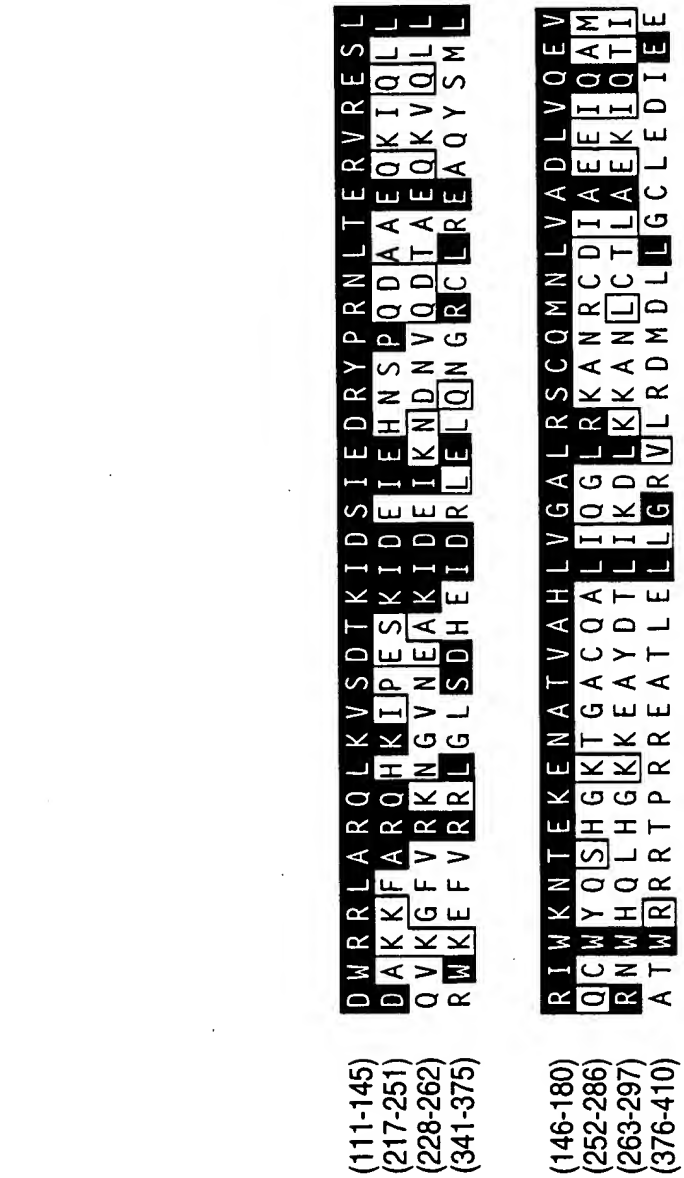
hFADD (111-145) DWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESL
rFas (217-251) DAKKFARQHKIPESKIDEIEHNSPQDAAEQKIQLL
hFas (228-262) QVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLL
hTNFR-1 (341-375) RWKEFVRRLGLSDHEIDRLELQNGRCLRESAQYSML
hFADD (146-180) RIWKNTEKENATVAHLVGALRSCQMNLVADLVQEV
rFas (252-286) QCWYQSHGKTGACQALIQGLRKANRCDIAEEIQAM
hFas (263-297) RNWHQLHGKEAYDTLIKDLKKANLCTLAEKIQTI
hTNFR-1 (376-410) ATWRRTPRREATLELLGRVLRDMDLLGCLEDIEE

FIG. 2C

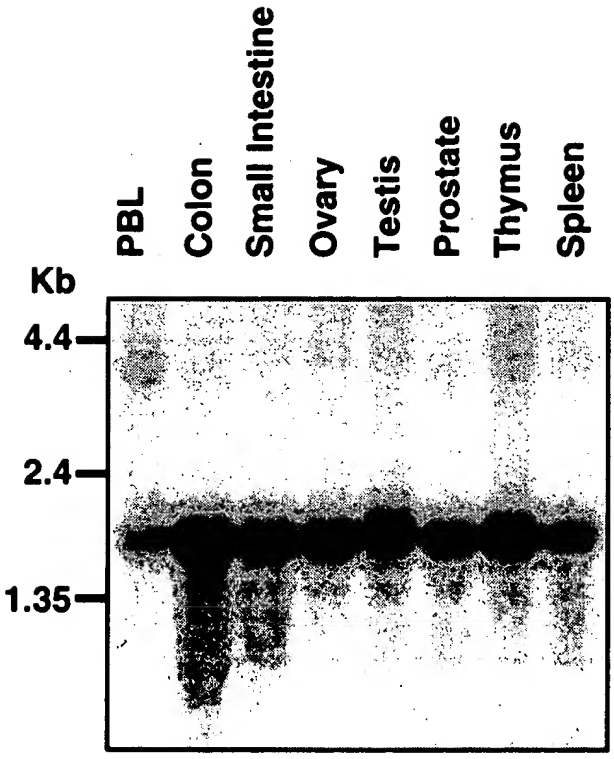
PBL
Colon
Small Intestine
Ovary
Testis
Prostate
Thymus
Spleen
Kb
4.4
2.4
1.35

FIG. 3A

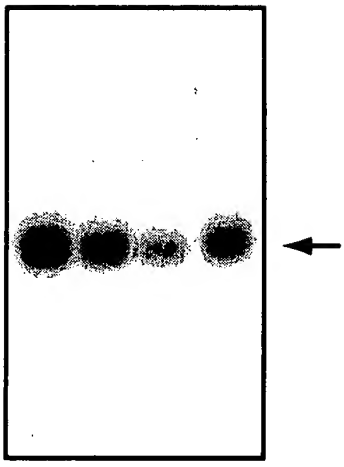
Kidney
Liver
Lung
Brain

FIG. 3B

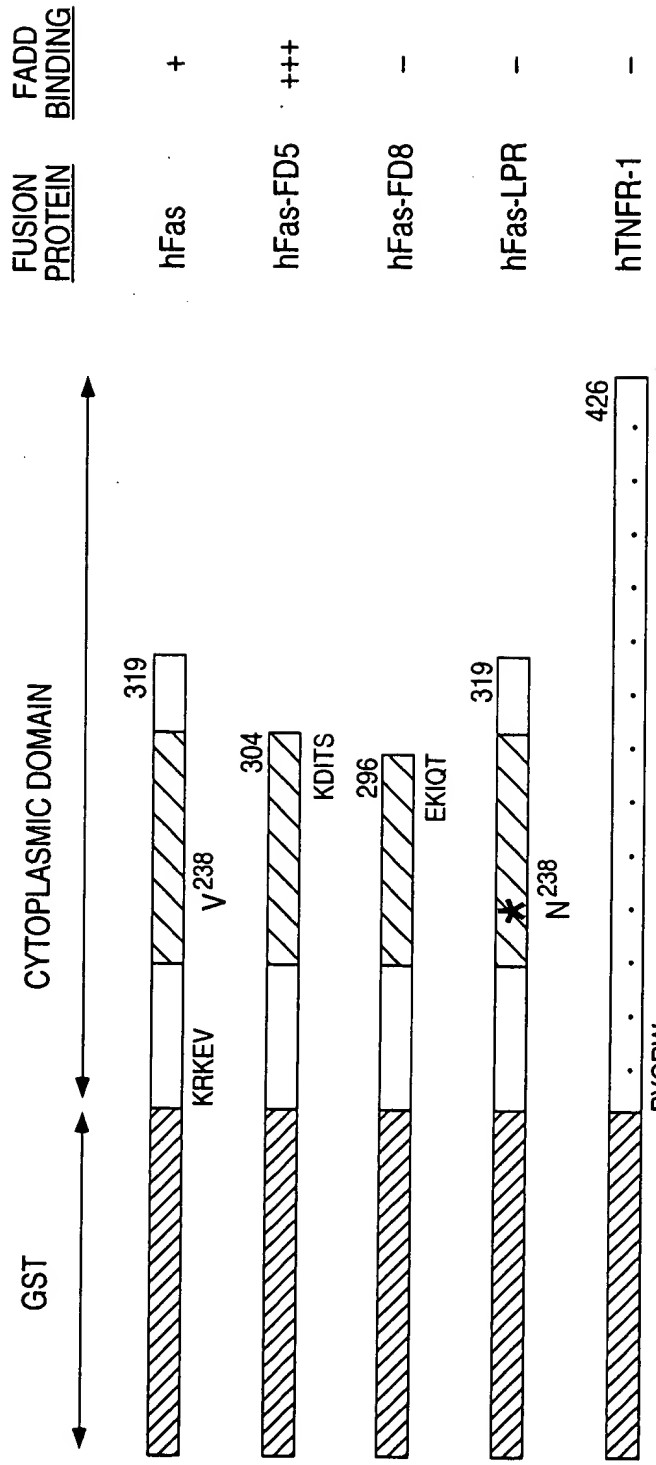
FUSION PROTEIN
FADD BINDING
hFas +
hFas-FD5 +++
hFas-FD8 –
hFas-LPR –
hTNFR-1 –
CYTOPLASMIC DOMAIN
GST
319
KRKEV
V 238
304
KDITS
296
EKIQT
319
N 238
426
RYQRW

FIG. 4A

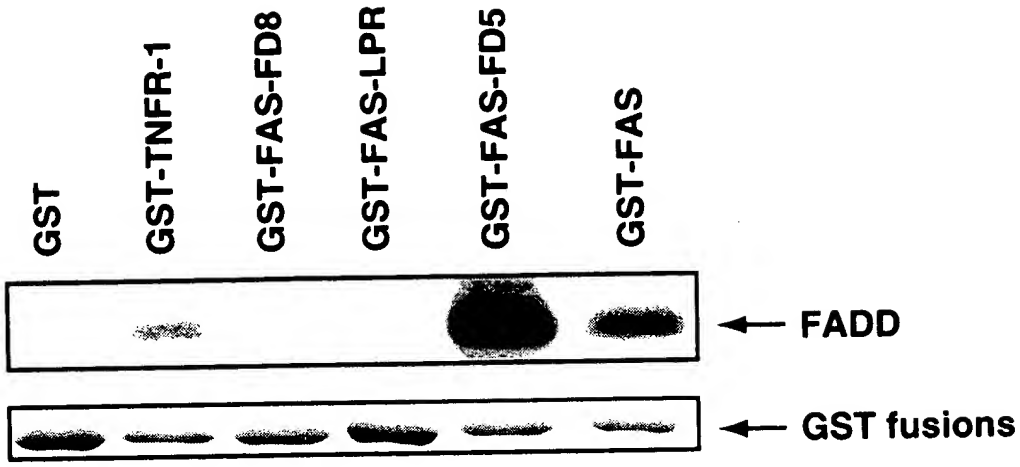
GST
GST-TNFR-1
GST-FAS-FD8
GST-FAS-LPR
GST-FAS-FD5
GST-FAS
FADD
GST fusions

FIG. 4B

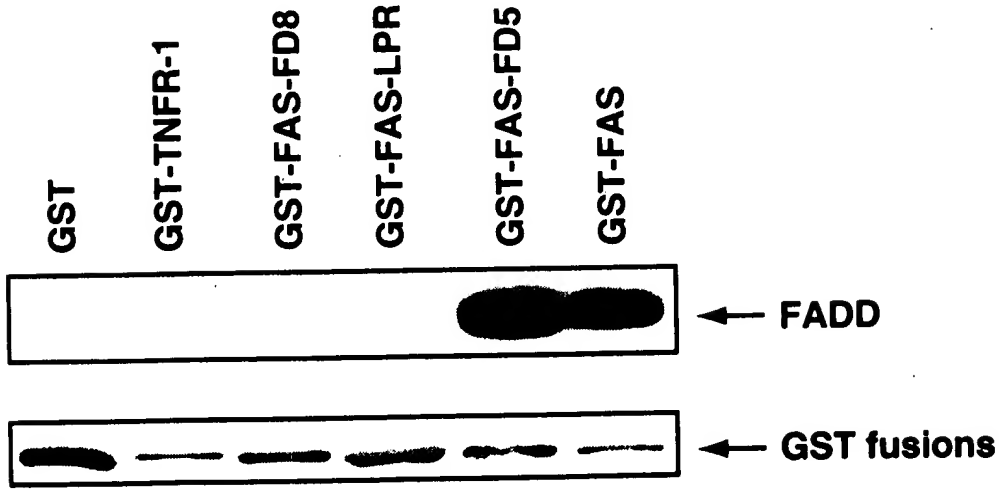
GST
GST-TNFR-1
GST-FAS-FD8
GST-FAS-LPR
GST-FAS-FD5
GST-FAS
FADD
GST fusions

FIG. 4C

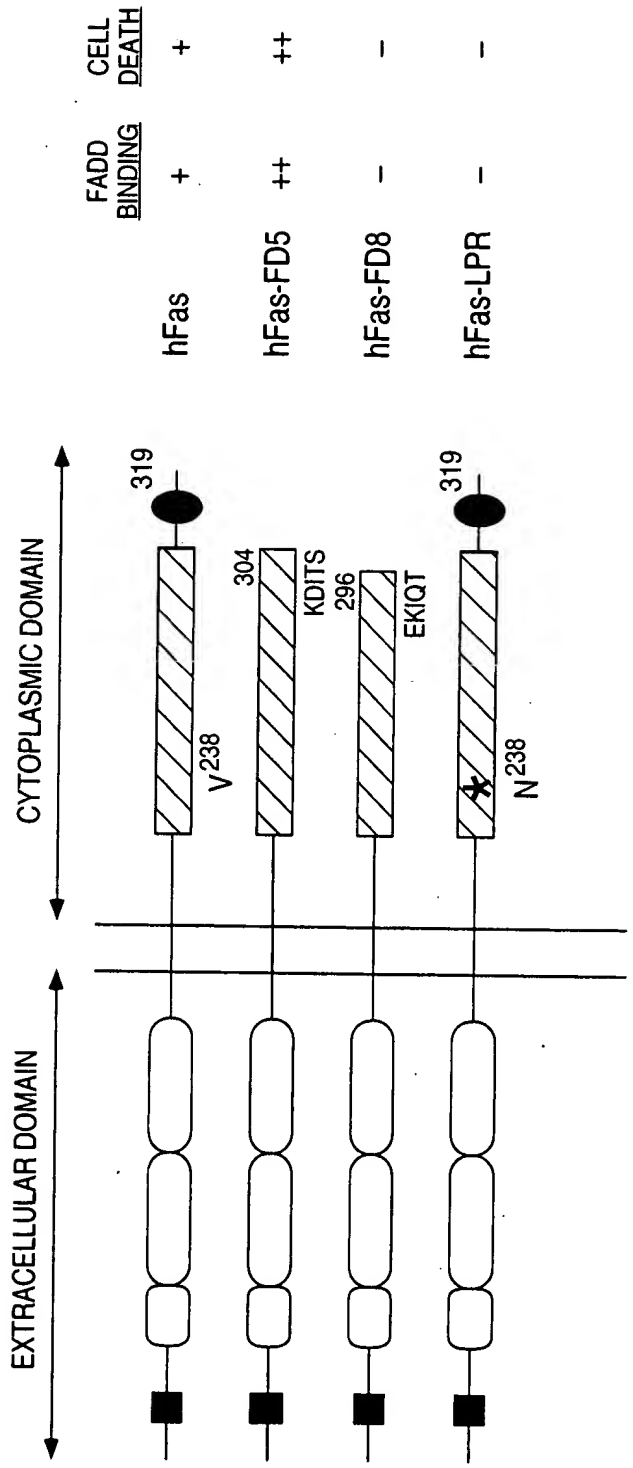
FADD BINDING
CELL DEATH
hFas + +
hFas-FD5 ++ ++
hFas-FD8 – –
hFas-LPR – –
CYTOPLASMIC DOMAIN
EXTRACELLULAR DOMAIN
319
V238
304
KDITS
296
EKIQT
319
N238

FIG. 5A

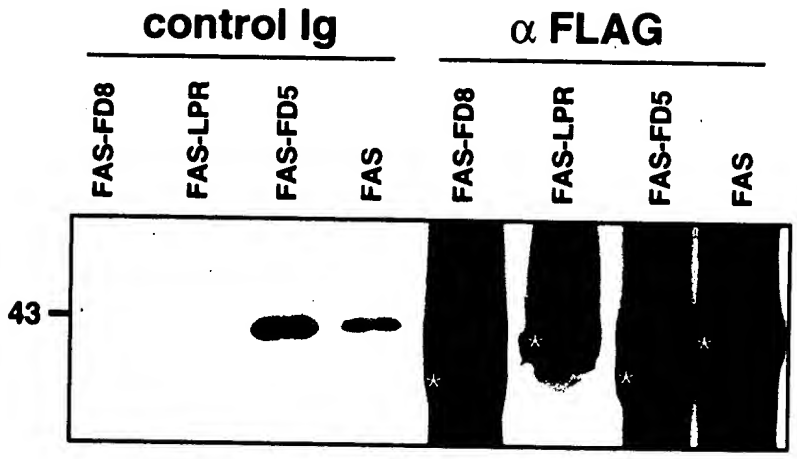
control Ig
α FLAG
FAS-FD8
FAS-LPR
FAS-FD5
FAS
FAS-FD8
FAS-LPR
FAS-FD5
FAS
43

FIG. 5B

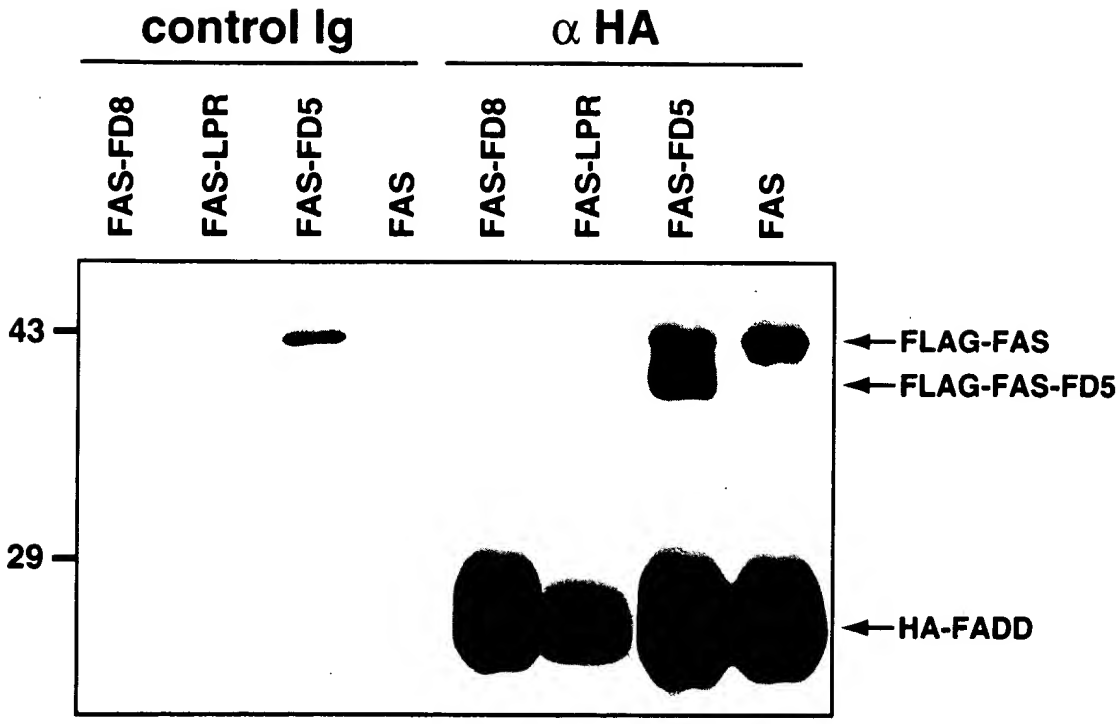
control Ig
α HA
FAS-FD8
FAS-LPR
FAS-FD5
FAS
FAS-FD8
FAS-LPR
FAS-FD5
FAS
43
29
FLAG-FAS
FLAG-FAS-FD5
HA-FADD

FIG. 5C

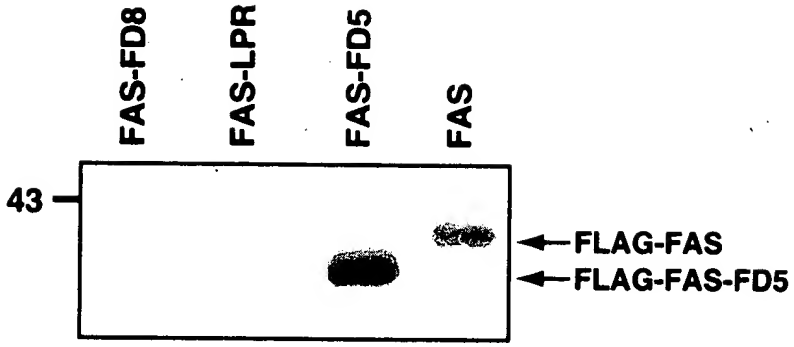

FIG. 5D

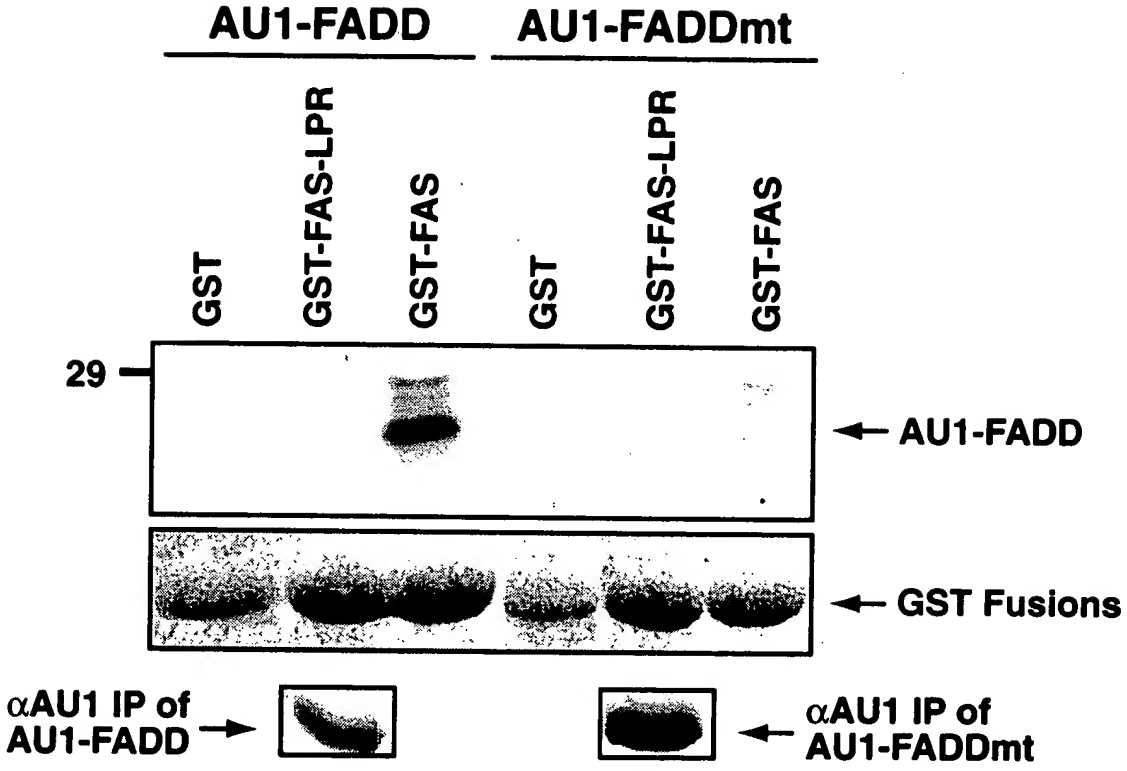
AU1-FADD
AU1-FADDmt
GST
GST-FAS-LPR
GST-FAS
GST
GST-FAS-LPR
GST-FAS
29
AU1-FADD
GST Fusions
αAU1 IP of AU1-FADD
αAU1 IP of AU1-FADDmt

FIG. 6

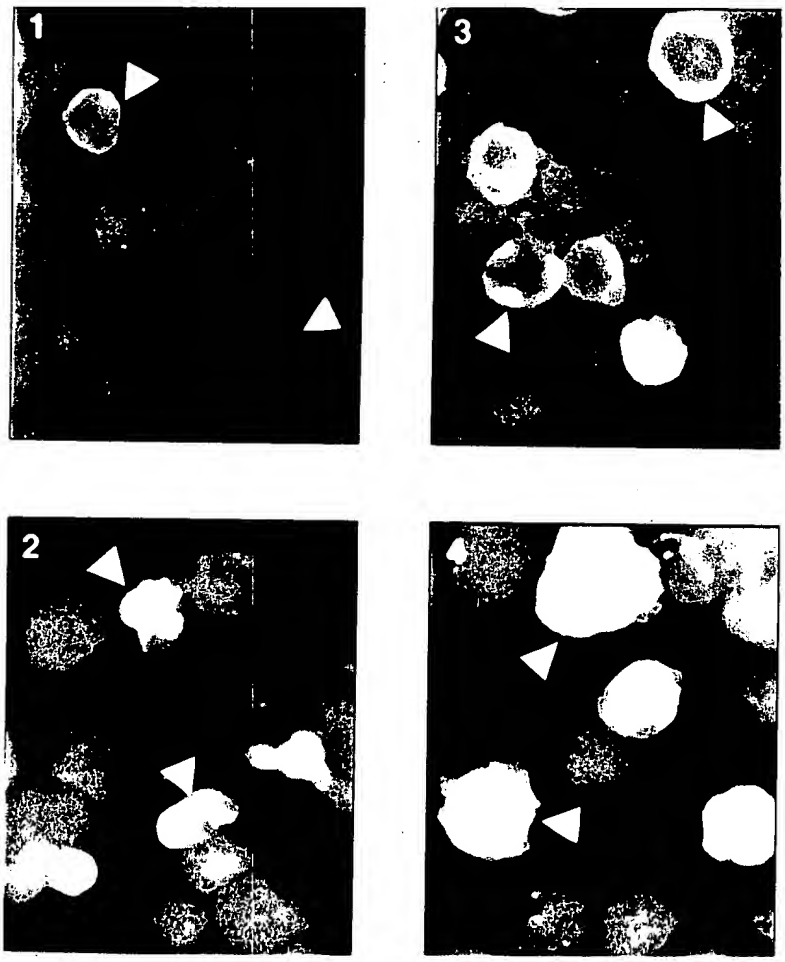

FIG. 7A

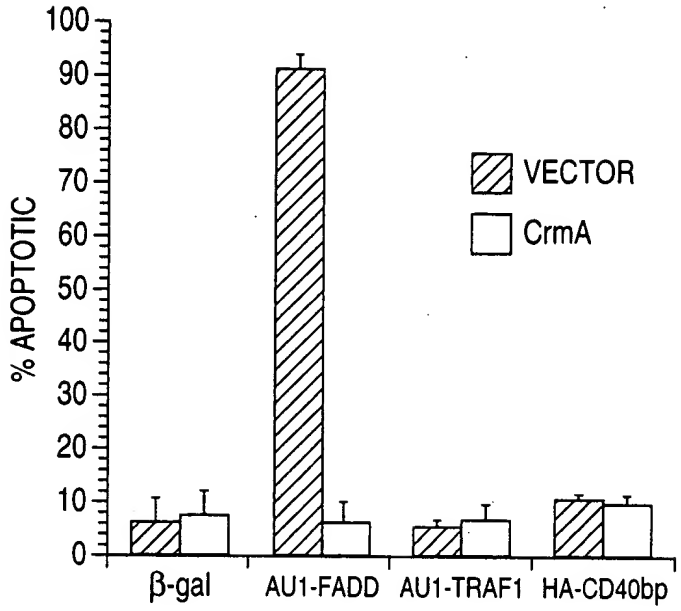
100
90
80
70
60
50
40
30
20
10
0
% APOPTOTIC
VECTOR
CrmA
β-gal
AU1-FADD
AU1-TRAF1
HA-CD40bp

FIG. 7B

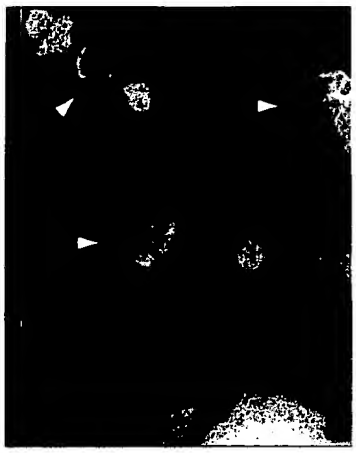

FIG. 7C

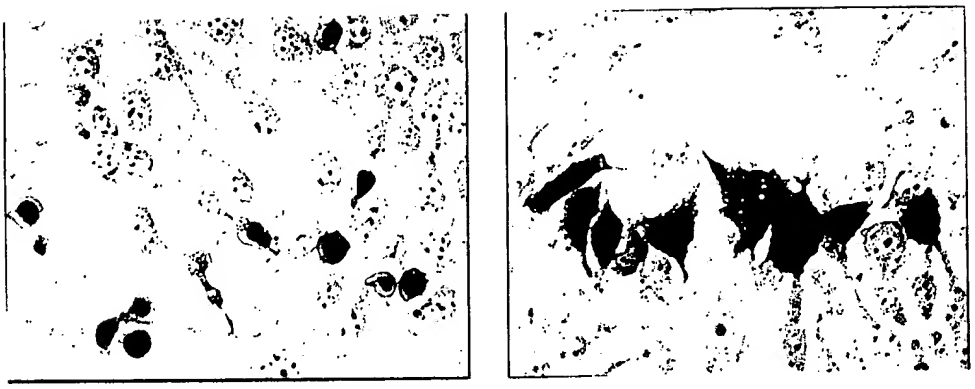

FIG. 8A

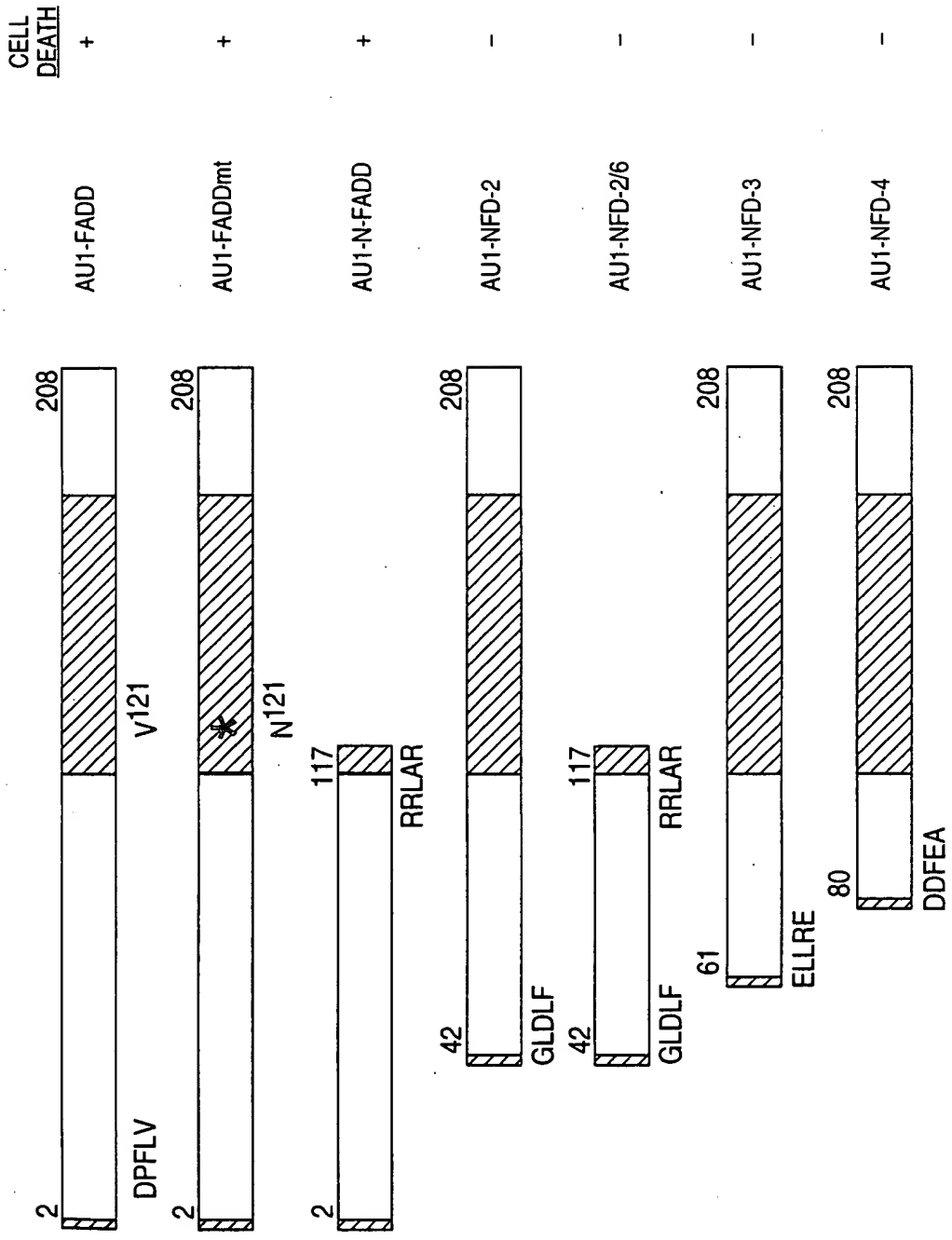
CELL DEATH
AU1-FADD
+
208
2
DPFLV
V121
AU1-FADDmt
+
208
2
N121
AU1-N-FADD
+
117
2
RRLAR
AU1-NFD-2
-
208
42
GLDLF
AU1-NFD-2/6
-
117
42
GLDLF
RRLAR
AU1-NFD-3
-
208
61
ELLRE
AU1-NFD-4
-
208
80
DDFEA

FIG. 8B